

AAGTCAACAA AGATGGAGCA CTGGCGTTGC TCCCAAAACA GCAGGAGAAC
 GGCGACCGGC CGGAGAAGGC TGGCGCCCCT GAAACCAGCA AGGAATACG
 CCCAGGTGTC CCGGGTGATG GATAACCACA TCCTGGTGTT AGTGCAGGAT
 CCGCGAGCTC GAAACGTGGC TCCGTTTGAA GAACCAACCA AGGAGACCCC
 GCCATCCCGG CCGCAGAATC CAGCTGCGAA AGACCTGGCC G/AGCTTCACCA
 CGGCCCCGGG CCACTGCAGA CACCCGCTGG GTGGGCTGGA TTACCTCGAT
 CCCGCAGGCT TTATGCACTC CTTTCAGTGA GAGCTTGGTT CATGGGATGA
 TGGGTTACAA GGTGGGGTTT TTTTCAGGTC GCACTACGTG AAATGCACTC
 TACCAGAGAA AGCTCGAAAA TGGGGTTAGA ATGACACTAC CCAGACTCAC
 AGTTCACTCC TCTTCATGCT CCATTTTCAA CCACTTGCCTCTT

G/A=G or A at polymorphic site

Fig. 1

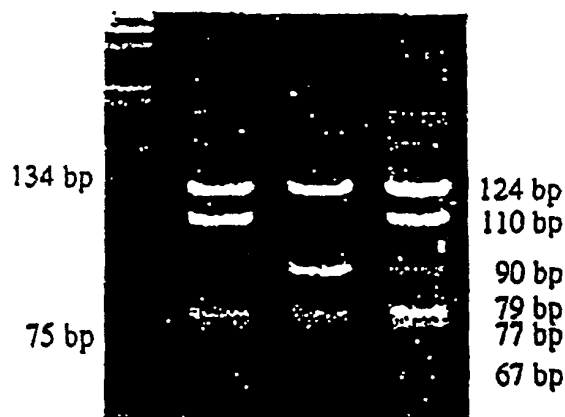


Fig. 2

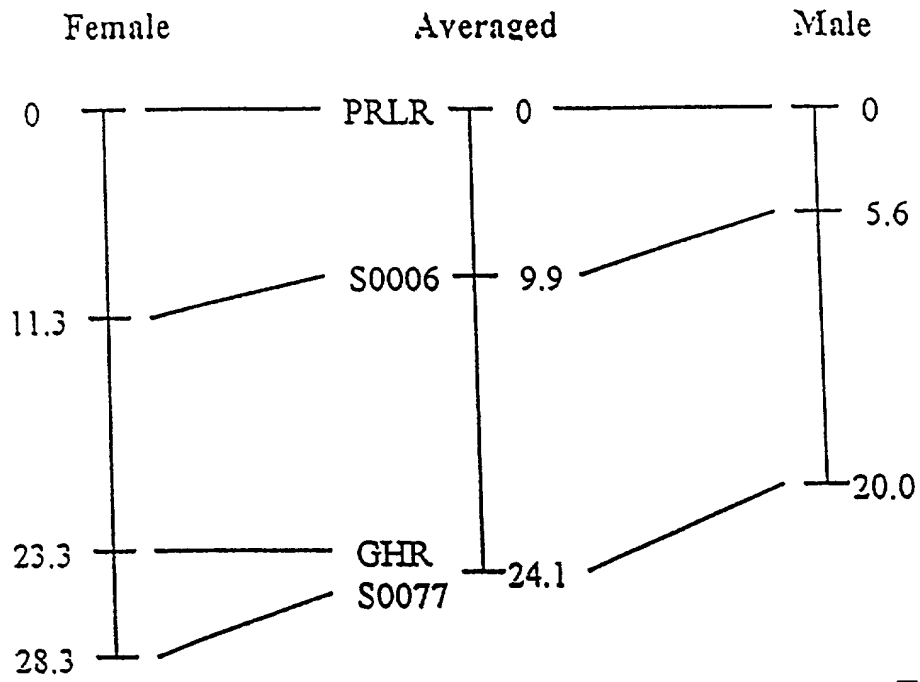


Fig. 3

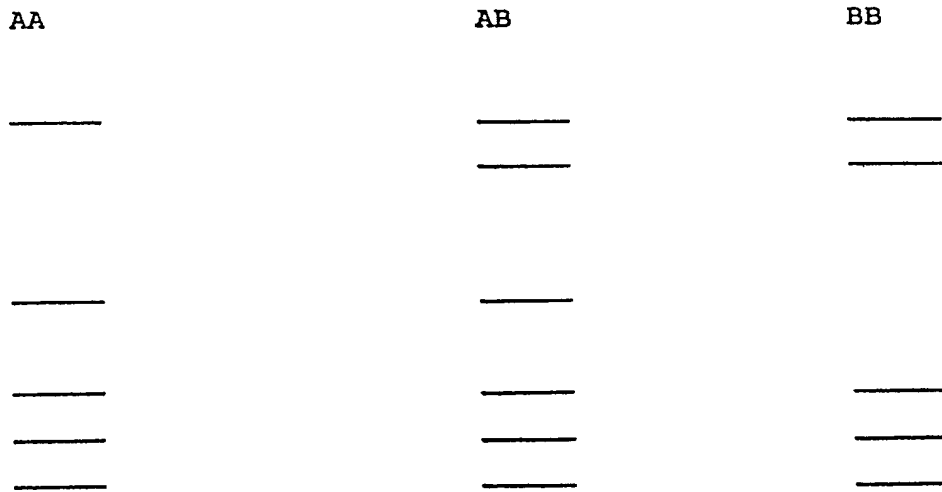


Fig. 4

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1  GATTATTGTC TGGGCAGTGG ----- TCTTCTCTGT CTATCNACCC CCCTCCCATT 60
61 CATGGCTCTC AGGGTATAAT GGCCAAAAAA AAGACAAGAC AAAAATGATG GAAACCTACA 120
121 GATAATTYAA GCACCTCATT TTGCCATTAG CTGCATTAGC CATAAAAAAA A----- 180
181 -----AAAAA AAAACCTTTT CTCAGTGCTA GAAAAAACA GAATAGACTC ATTTGAAACT 240
241 GATCTTCTCT CTACCAAAGG GAGTAGCGCA GTTGTGAAAT AGTAAACGTC TGACAAGAAC 300
301 AGCAAATAAT CCCACTAGTA ATTTCAGAAT CCGCCTCCTC AATTAGCCAG AATTCACTGT 360
361 GATGCTGGCC TCTATAATTA TTATTTGTCT TCACCACTGA TTAGTTTCAC ATCATGAAAA 420
421 TTGCATGTCA TTTAGTTTCA CRTAGCCTCA GAACCAACCC TAATTCCTAC CTGCCATATC 480
481 CCTGTAGCAG CTATTCGAAG ATCACAAGGT GGGAACATGT GTYATTTATC TTTTCTCTTA 540
541 CATTATTTTA GAGCATGGTG GCCTGCATCC ----- GGGCCAAAAA TAAAAGGATT 600
    
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Fig. 5

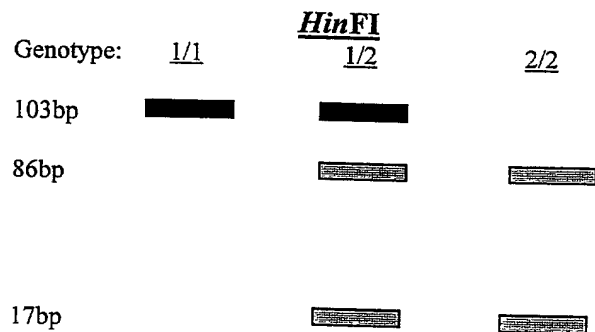


Fig. 6

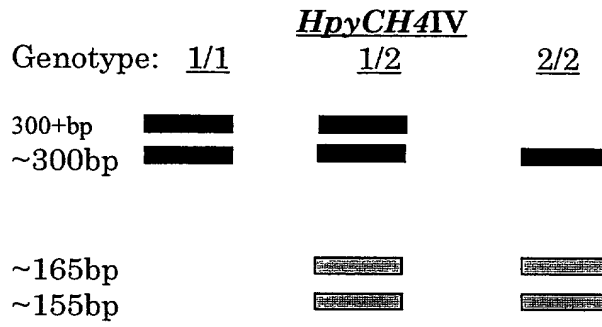


Fig. 7

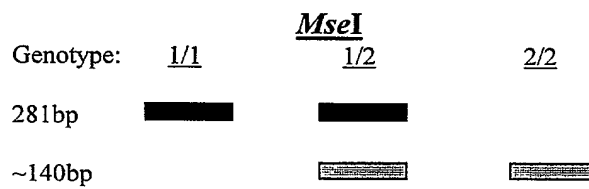


Fig. 8

Sequence 5' to 3' for porcine PRLR Sequence

GTACACACAC ACACACACAC ACACACACAC ACACACCACC GTTAAGCTNT CTTTCTGAAT CATGCCNACC
 CGAGGGCCAC CCATAGAGGA GTGTGGTGA GGGTGCCTTG GCACTTCTGA GCCCTGCATC CCTACACCCA
 CTAGCCTCAA GATGTCATC CCTGCCCTGG CCCCCACCCA TCTGCTTCTG TCACCAGCAG AATGGTCCAG
 TCATTGAGCG GACCTTCATA TTGACTCCAG TGGCTTCTGG CTTTTTCTAG GACAGTCACC TCCGGGAAAA
 CCTGAGATCT TCAAATGTCG TTCTCCCGAA AAGGAAACAT TCGCCTGCTG GTGGAAGCCG GGGGCGGATG
 GAGGACTTCC TACCAACTAG ACGCTGACTT ACCACAAGGA AGGGTAAGCA TTCGCGTGTC TCCCAACAAA
 CCACACGAGT GTTCTCTCTC TGTGGGCCAG AGGAACACTG CTTCTGGGTT AGAACTGCCT CGCTTTGGAG
 TTCCCGTCAT GGCTCAGTGG TAACGAATC

Human exon 4

gacagttacctcctgg aaaacctgag atctttaaat gtcgttctcc caataaggaa acattcacct
 gctggtggag gcctgggaca gatggaggac ttcctaccaa ttattcactg acttaccaca
 ggggaagg

Alignment

	Exon 4
Hsap	g a c a g t t a c c t c c t g g a a a c c t g a g a t c t t t a a a t G Q L P P G K P E I F K
pig	? a c a g t c a c c t c c g g g a a a c c t g a g a t c t t c a a a t S P F
Hsap	g t c g t t c t c c c a a t a a g g a a a c a t t c a c c t g c t g g t C R S P N K E T F T
pig	g t c g t t c t c c c g a a a a g g a a a c a t t c g c c t g c t g g t E A
Hsap	g g a g g c c t g g g a c a g a t g g a g g a c t t c c t a c c a a t t R P G T D G G L P T N
pig	g g a a g c c g g g g g c g g a t g g a g g a c t t c c t a c c a a c t K P A N
Hsap	a t t c a c t g a c t t a c c a c a g g g a a g g Y S L T Y H R E G
pig	? g a c g c t g a c t t a c c a c a a g g a a g g ** T K

Fig. 9